AMENDMENTS TO THE CLAIMS

Please amend the claims as shown below.

1. (Six times amended) A mutant prenyl diphosphate synthase having [a modified] an amino acid sequence modified from the amino acid sequence of SEQ ID NO:1 wherein the amino acid sequence modifications are selected from the group consisting of:

threonine modified to phenylalanine at position 78 and histidine modified to alanine at position 81;

threonine modified to phenylalanine at position 78 and histidine modified to leucine at position 81;

phenylalanine modified to tyrosine at position 77, threonine modified to phenylalanine at position 78 and histidine modified to leucine at position 81;

phenylalanine modified to tyrosine at position 77, threonine modified to phenylalanine at position 78 and histidine modified to alanine at position 81; and,

phenylalanine modified to tyrosine at position 77, threonine modified to serine at position 78, valine modified to isoleucine at position 80, isoleucine modified to leucine at position 84 and proline and serine inserted sequentially between position 84 and position 85

[wherein

said mutant prenyl diphosphate synthase comprises an aspartic acid-rich domain having the sequence, $D_1D_2X_1X_2(X_3X_4)D_3$, in region II of said mutant prenyl diphosphate synthase

wherein each of D_1, D_2, and D_3 denote an aspartic acid residue; X_1, X_2 , X_3, and X_4 are each independently any amino acid and X_3 and X_4 are each optionally independently present in the aspartic acid rich domain,

and wherein said mutant prenyl diphosphate synthase comprises (1) at least one amino acid substitution, said at least one amino acid substitution located at at least one amino acid position selected from (a) an amino acid between D_1 and the amino acid residue at the fifth position upstream of D_1 and (b) the amino acid residue located one amino acid position upstream of D_3; (2) at least one additional amino acid inserted between D_3 and the first amino acid upstream of D_3; or a combination of (2) (1) and (3) (2);

wherein said mutant prenyl diphosphate synthase synthesizes prenyl diphosphate which is shorter than prenyl diphosphate synthesized by a corresponding wild-type enzyme].

2. (Three times amended) A mutant prenyl diphosphate synthase according to claim 1 wherein said mutant has [the enzymatic activities and] the thermostability of wild type prenyl diphosphate synthase and synthesizes about as much or more prenyl diphosphate than the amount of prenyl diphosphate synthesized by the wild type prenyl diphosphate synthase under similar conditions.

3. (Amended) A mutant enzyme according to claim 1 wherein the reaction product of the mutant prenyl diphosphate synthase is farnesyl diphosphate.

4. (Amended) A mutant enzyme according to claim 1 wherein the prenyl diphosphate synthase is [of the homodimer-type] a homodimer.

5. (Amended) A mutant enzyme according to claim 1 wherein the prenyl diphosphate synthase is [derived from] an archaea prenyl diphosphate synthase.

6. (Amended) A mutant enzyme according to claim 1 wherein the prenyl diphosphate synthase is [derived from] *Sulfolobus acidocaldarius* prenyl diphosphate synthase.

7. (Amended) A mutant enzyme according to claim 1 wherein the prenyl diphosphate synthase is [a] at least as thermostable as the corresponding wild-type prenyl diphosphate synthase [enzyme].

8-10. (Canceled).

11. (Original) A DNA encoding an enzyme according to claim 1.

12. (Original) An RNA transcribed from a DNA according to claim 11.

13. (Original) A recombinant vector comprising a DNA according to claim 11.

14. (Original) A host organism transformed with a recombinant vector according to claim 13.

15. (Original) A process for producing a mutant enzyme according to claim 1, said method comprising the steps of culturing a host transformed with an expression vector comprising a DNA coding for the mutant enzyme and of harvesting the expression product from the culture.

16. (Amended) A process for producing a prenyl diphosphate having not more than 15 carbons comprising the step of bringing an enzyme according to [claim] any one of claims 1

[or any of claims 2] to 7 [10] or an enzyme produced by the method according to claim 15 into contact with a substrate selected from the group consisting of isopentenyl diphosphate, dimethylallyl diphosphate, and geranyl diphosphate.

17-48. (Canceled).

49. The mutant prenyl diphosphate synthase of claim 1 wherein said amino acid sequence modifications consist of threonine modified to phenylalanine at position 78 and histidine modified to alanine at position 81.

50. The mutant prenyl diphosphate synthase of claim 1 wherein said amino acid sequence modifications consist of threonine modified to phenylalanine at position 78 and histidine modified to leucine at position 81.

51. The mutant prenyl diphosphate synthase of claim 1 wherein said amino acid sequence modifications consist of phenylalanine modified to tyrosine at position 77, threonine modified to phenylalanine at position 78 and histidine modified to leucine at position 81.

52. The mutant prenyl diphosphate synthase of claim 1 wherein said amino acid sequence modifications consist of phenylalanine modified to tyrosine at position 77, threonine modified to phenylalanine at position 78 and histidine modified to alanine at position 81.

53. The mutant prenyl diphosphate synthase of claim 1 wherein said amino acid sequence modifications consist of phenylalanine modified to tyrosine at position 77, threonine modified to serine at position 78, valine modified to isoleucine at position 80, isoleucine modified to leucine at position 84 and proline and serine inserted sequentially between position 84 and position 85.

54. A mutant prenyl diphosphate synthase having an amino acid sequence modified from the amino acid sequence of a wild-type prenyl diphosphate synthase

wherein said sequence of said mutant prenyl diphosphate synthase and said sequence of said wild-type prenyl diphosphate synthase comprise an aspartic acid rich domain having the sequence $D_1D_2X_1X_2(X_3X_4)D_3$;

wherein each of D_1, D_2, and D_3 denote an aspartic acid residue; X_1, X_2 , X_3, and X_4 are each independently any amino acid and X_3 and X_4 are each optionally independently present in the aspartic acid rich domain;

wherein said sequence of said mutant prenyl diphosphate synthase is modified from said sequence of said wild-type prenyl diphosphate synthase only in the amino acid sequence beginning at the position five amino acids upstream of said aspartic acid rich domain and ending at the aspartic acid in the position of D_3 and wherein said modification comprises (1) at least one amino acid substitution, said at least one amino acid substitution located at at least one amino acid position selected from (a) an amino acid between D_1 and the amino acid residue at the fifth position upstream of D_1 and (b) the amino acid residue located one amino acid position upstream of D_3; (2) at least one additional amino acid inserted between D_3 and the first amino acid upstream of D_3; or (3) a combination of (1) and (2);

wherein said mutant prenyl diphosphate synthase synthesizes a greater amount of a prenyl diphosphate of a first chain length than is synthesized by a corresponding wild-type prenyl diphosphate synthase;

wherein said first chain length of prenyl diphosphate is shorter than a second chain length of prenyl diphosphate synthesized by said wild-type prenyl diphosphate synthase;

wherein said wild-type prenyl diphosphate synthase synthesizes said prenyl diphosphate of said second chain length in greater abundance than said wild-type prenyl diphosphate synthesizes said prenyl diphosphate of said first chain length; and

wherein said wild-type prenyl diphosphate synthase may or may not synthesize said prenyl diphosphate of said first chain length.

55. A DNA encoding an enzyme according to claim 54.

56. A process for producing a mutant enzyme according to claim 54, said method comprising the steps of culturing a host transformed with an expression vector comprising a DNA coding for the mutant enzyme and of harvesting the expression product from the culture.

57. A process for producing a prenyl diphosphate having not more than 15 carbons comprising the step of bringing an enzyme according to claim 54 or an enzyme produced by the method according to claim 56 into contact with a substrate selected from the group consisting of isopentenyl diphosphate, dimethylallyl diphosphate, and geranyl diphosphate.

58. A mutant prenyl diphosphate synthase having an amino acid sequence modified from the amino acid sequence of a wild-type prenyl diphosphate synthase

wherein said sequence of said mutant prenyl diphosphate synthase and said sequence of said wild-type prenyl diphosphate synthase comprise an aspartic acid rich domain having the sequence $D_1D_2X_1(X_2X)_3X_4D_3$;

wherein each of D_1, D_2, and D_3 denote an aspartic acid residue; X_1, X_2, X_3, and X_4 are each independently any amino acid and X_2 and X_3 are each optionally independently present in the aspartic acid rich domain;

wherein said sequence of said mutant prenyl diphosphate synthase is modified from said sequence of said wild-type prenyl diphosphate synthase only in the amino acid sequence beginning at the position five amino acids upstream of said aspartic acid rich domain and ending at the aspartic acid in the position of D_3 and wherein said modification comprises (1) at least one amino acid substitution, said at least one amino acid substitution located at at least one amino acid position selected from (a) an amino acid between D_1 and the amino acid residue at the fifth position upstream of D_1 and (b) the amino acid residue located one amino acid position downstream of D_2; (2) at least one additional amino acid inserted between the first amino acid downstream of D_2 and the first amino acid upstream of D_3; or (3) a combination of (1) and (2);

wherein said mutant prenyl diphosphate synthase synthesizes a greater amount of a prenyl diphosphate of a first chain length than is synthesized by a corresponding wild-type prenyl diphosphate synthase;

wherein said first chain length is shorter than a second chain length of prenyl diphosphate synthesized by said wild-type prenyl diphosphate synthase;

wherein said wild-type prenyl diphosphate synthase synthesizes said prenyl diphosphate of said second chain length in greater abundance than said wild-type prenyl diphosphate synthesizes said prenyl diphosphate of said first chain length; and,

wherein said wild-type prenyl diphosphate synthase may or may not synthesize any of said prenyl diphosphate of said first chain length.

59. A DNA encoding an enzyme according to claim 58.

60. A process for producing a mutant enzyme according to claim 58, said method comprising the steps of culturing a host transformed with an expression vector comprising a DNA coding for the mutant enzyme and of harvesting the expression product from the culture.

61. A process for producing a prenyl diphosphate having not more than 15 carbons comprising the step of bringing an enzyme according to claim 58 or an enzyme produced by the method according to claim 60 into contact with a substrate selected from the group consisting of isopentenyl diphosphate, dimethylallyl diphosphate, and geranyl diphosphate.

62. A mutant prenyl diphosphate synthase having an amino acid sequence modified from the amino acid sequence of a wild-type prenyl diphosphate synthase only within region II of the amino acid sequence of said wild-type prenyl diphosphate synthase wherein region II of said amino acid sequence of said wild-type prenyl diphosphate synthase is 45% homologous with the sequence consisting of positions 72 through 93 of SEQ ID NO:1; and

wherein said sequence of said mutant prenyl diphosphate synthase and said sequence of said wild-type prenyl diphosphate synthase comprise an aspartic acid rich domain having the sequence $D_1D_2X_1X_2(X_3X_4)D_3$;

wherein each of D_1, D_2, and D_3 denote an aspartic acid residue; X_1, X_2, X_3, and X_4 are each independently any amino acid and X_3 and X_4 are each optionally independently present in the aspartic acid rich domain;

wherein said aspartic acid rich domain comprised within said sequence of said wild-type prenyl diphosphate synthase is comprised within said region II of said sequence of said wild-type prenyl diphosphate synthase; and

wherein the modification of said region II of said sequence of said wild-type prenyl diphosphate synthase is (1) at least one amino acid substitution, said at least one amino acid substitution located at at least one amino acid position selected from (a) an amino acid between D_1 and the amino acid residue at the fifth position upstream of D_1 and (b) the amino acid residue located one amino acid position upstream of D_3; (2) at least one additional amino acid inserted between D_3 and the first amino acid upstream of D_3; or (3) a combination of (1) and (2),

wherein said mutant prenyl diphosphate synthase synthesizes a greater amount of a prenyl diphosphate of a first chain length than is synthesized by a corresponding wild-type prenyl diphosphate synthase;

wherein said first chain length of prenyl diphosphate is shorter than a second chain length of prenyl diphosphate synthesized by said wild-type prenyl diphosphate synthase;

wherein said wild-type prenyl diphosphate synthase synthesizes said prenyl diphosphate of said second chain length in greater abundance than said wild-type prenyl diphosphate synthesizes said prenyl diphosphate of said first chain length; and

wherein said wild-type prenyl diphosphate synthase may or may not synthesize said prenyl diphosphate of said first chain length.

63. A mutant prenyl diphosphate synthase having an amino acid sequence modified from the amino acid sequence of a wild-type prenyl diphosphate synthase only within region II of the amino acid sequence of said wild-type prenyl diphosphate synthase wherein region II of said amino acid sequence of said wild-type prenyl diphosphate synthase is 45% homologous with the sequence consisting of positions 72 through 93 of SEQ ID NO:1; and

wherein said sequence of said mutant prenyl diphosphate synthase and said sequence of said wild-type prenyl diphosphate synthase comprise an aspartic acid rich domain having the sequence $D_1D_2X_1(X_2X_3)X_4D_3$;

wherein each of D_1, D_2, and D_3 denote an aspartic acid residue; X_1, X_2, X_3, and X_4 are each independently any amino acid and X_2 and X_3 are each optionally independently present in the aspartic acid rich domain;

wherein said aspartic acid rich domain comprised within said sequence of said wild-type prenyl diphosphate synthase is comprised within said region II of said sequence of said wild-type prenyl diphosphate synthase; and

wherein the modification of said region II of said sequence of said wild-type prenyl diphosphate synthase is (1) at least one amino acid substitution, said at least one amino acid substitution located at at least one amino acid position selected from (a) an amino acid between D_1 and the amino acid residue at the fifth position upstream of D_1 and (b) the amino acid residue located one amino acid position downstream of D_2; (2) at least one additional amino acid inserted between the first amino acid downstream of D_2 and the first amino acid upstream of D_3; or (3) a combination of (1) and (2);

wherein said mutant prenyl diphosphate synthase synthesizes a greater amount of a prenyl diphosphate of a first chain length than is synthesized by a corresponding wild-type prenyl diphosphate synthase;

wherein said first chain length is shorter than a second chain length of prenyl diphosphate synthesized by said wild-type prenyl diphosphate synthase;

wherein said wild-type prenyl diphosphate synthase synthesizes said prenyl diphosphate of said second chain length in greater abundance than said wild-type prenyl diphosphate synthesizes said prenyl diphosphate of said first chain length; and,

wherein said wild-type prenyl diphosphate synthase may or may not synthesize any of said prenyl diphosphate of said first chain length.

STATUS OF CLAIMS AND SUPPORT FOR CLAIM CHANGES

1. (Pending) The current amendment to claim 1 is supported, for example, by Examples 4 and 5 and Figure 3 of the specification. Five embodiments of the current invention are disclosed as recombinant gene constructs in Example 4 and demonstrated to synthesize farnesyl diphosphate having a shorter chain length than the native gene in Example 5 and Figure 3 of the specification. Col. 12, line 1 through Col. 14, line 16.

2. (Pending)

3. (Pending)

4. (Pending)

5. (Pending)

6. (Pending)

7. (Pending)

8-10. (Canceled)

11. (Pending)

12. (Pending)

13. (Pending)

14. (Pending)

15. (Pending)

16. (Pending)

17-48. (Canceled)

49. (Pending) Claim 49 is presented as new. Support may be found for claim 49, for example, in the substitution-mutated pBs-SacGGPS plasmid containing SEQ ID NO:9 disclosed in Example 4 and the functional enzyme expressed from the plasmid as disclosed in Example 5 and Figure 3.

50. (Pending) Claim 50 is new. Support may be found for claim 50, for example, in the substitution-mutated pBs-SacGGPS plasmid containing SEQ ID NO:10 disclosed in Example 4 and the functional enzyme expressed from the plasmid as disclosed in Example 5 and Figure 3.

51. (Pending) Claim 51 is presented as new. Support may be found for claim 51, for example, in the substitution-mutated pBs-SacGGPS plasmid containing SEQ ID NO:11

disclosed in Example 4 and the functional enzyme expressed from the plasmid as disclosed in Example 5 and Figure 3.

52. (Pending) Claim 52 is presented as new. Support may be found for claim 52, for example, in the substitution-mutated pBs-SacGGPS plasmid containing SEQ ID NO:12 disclosed in Example 4 and the functional enzyme expressed from the plasmid as disclosed in Example 5 and Figure 3.

53. (Pending) Claim 53 is presented as new. Support may be found for claim 53, for example, in the substitution-mutated pBs-SacGGPS plasmid containing SEQ ID NO:13 disclosed in Example 4 and the functional enzyme expressed from the plasmid as disclosed in Example 5 and Figure 3.

54. (Pending) Claim 54 is presented new. Claim 54 corresponds to original claim 1 as amended through the Amendment with RCE filed June 2, 2006 in the above-captioned reissue application and contains current changes directed to a mutant having modifications only within the sequence beginning five amino acids upstream of the aspartic acid-rich domain through and including the aspartic acid-rich domain of a wild-type prenyl diphosphate synthase where all other portions of the sequence of the mutant prenyl diphosphate synthase are homologous with the amino acid sequence of its corresponding wild-type prenyl diphosphate synthase. Support for claim 54 may be found, for example, at column 4, line 60, through column 5, line 7; column 5, line 66, through column 6, line 17; Example 1, in column 10; Example 4, in column 12; and, in Figure 1.

55. (Pending) Claim 55 is presented new. Claim 55 corresponds to original claim 11 and has been changed from original claim 11 to depend from new claim 54.

56. (Pending) Claim 56 is presented new. Claim 56 corresponds to original claim 15 and has been changed from original claim 15 to depend from new claim 54.

57. (Pending) Claim 57 is presented new. Claim 57 corresponds to original claim 16 and has been changed from original claim 16 to depend from new claim 54.

58. (Pending) Claim 58 is presented new. Claim 58 corresponds to claim 35 as presented in the Amendment with RCE filed June 2, 2006 in the above-referenced reissue application. In the presently pending Office Action, the Examiner informed Applicants that the proper designation for claim 35 was, in fact, claim 33. As such, new claim 58 corresponds to

claim 33 and is directed to a mutant having modifications only within the sequence beginning five amino acids upstream of the aspartic acid-rich domain through and including the aspartic acid-rich domain of a wild-type prenyl diphosphate synthase where all other portions of the sequence of the mutant prenyl diphosphate synthase are homologous with the amino acid sequence of its corresponding wild-type prenyl diphosphate synthase. Support for claim 58 may be found, for example, at column 4, line 60 through column 5, line 7; column 5, line 66 through column 6, line 17; column 6, lines 59 through 64, Example 2, in column 10; Example 4, in column 12 and in Figure 1.

59. (Pending) Claim 59 is presented new. Claim 59 corresponds to original claim 11 and has been changed from original claim 11 to depend from new claim 58.

60. (Pending) Claim 60 is presented new. Claim 60 corresponds to original claim 15 and has been changed from original claim 15 to depend from new claim 58.

61. (Pending) Claim 61 is presented new. Claim 61 corresponds to original claim 16 and has been changed from original claim 16 to depend from new claim 58.

62. (Pending) Claim 62 is presented new. Claim 62 corresponds to original claim 1 as amended through the Amendment with RCE filed June 2, 2006 in the above-captioned reissue application and contains current changes directed to a mutant having modifications only within region II of a wild-type prenyl diphosphate synthase where all other portions of the sequence of the mutant prenyl diphosphate synthase are homologous with the amino acid sequence of its corresponding wild-type prenyl diphosphate synthase. Region II is defined in the claim as the amino acid sequence of a wild-type prenyl diphosphate synthase enzyme having 45% homology with region II in SEQ ID NO:1. This definition of region II corresponds to the wild-type sequences disclosed in Figure 1 of the specification. Support for claim 62 may be found, for example, at column 4, line 60 through column 5, line 7; column 5, line 66 through column 6, line 17; Example 1, in column 10; Example 4, in column 12; and, in Figure 1.

63. (Pending) Claim 63 is presented new. Claim 63 corresponds to claim 35 as presented in the Amendment with RCE filed June 2, 2006 in the above-referenced reissue application. In the presently pending Office Action, the Examiner informed Applicants that the proper designation for claim 35 was, in fact, claim 33. As such, new claim 63 corresponds to claim 33 and is directed to a mutant having modifications only within region II of a wild-type

prenyl diphosphate synthase where all other portions of the sequence of the mutant prenyl diphosphate synthase are homologous with the amino acid sequence of its corresponding wild-type prenyl diphosphate synthase. Region II is defined in the claim as the amino acid sequence of a wild-type prenyl diphosphate synthase enzyme having 45% homology with region II in SEQ ID NO:1. This definition of region II corresponds to the wild-type sequences disclosed in Figure 1 of the specification. Support for claim 63 may be found, for example, at column 4, line 60 through column 5, line 7; column 5, line 66 through column 6, line 17; Example column 6, lines 59 through 64, Example 2, in column 10; Example 4, in column 12; and, in Figure 1.